

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/833,111

DATE: 05/02/2001
 TIME: 12:13:59

Input Set : A:\PF548SL.txt
 Output Set: N:\CRF3\05022001\I833111.raw

3 <110> APPLICANT: Rosen, Craig A.
 4 Haseltine, William A.
 6 <120> TITLE OF INVENTION: Albumin Fusion Proteins
 8 <130> FILE REFERENCE: PF548
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/833,111
 11 <141> CURRENT FILING DATE: 2001-04-12
 13 <150> PRIOR APPLICATION NUMBER: 60/229,358
 14 <151> PRIOR FILING DATE: 2000-04-12
 16 <150> PRIOR APPLICATION NUMBER: 60/256,931
 17 <151> PRIOR FILING DATE: 2000-12-21
 19 <150> PRIOR APPLICATION NUMBER: 60/199,384
 20 <151> PRIOR FILING DATE: 2000-04-25
 22 <160> NUMBER OF SEQ ID NOS: 72
 24 <170> SOFTWARE: PatentIn Ver. 2.1
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 23
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Artificial Sequence
 31 <220> FEATURE:
 32 <221> NAME/KEY: primer_bind
 33 <223> OTHER INFORMATION: primer useful to clone human growth hormone cDNA
 35 <400> SEQUENCE: 1
 36 cccaagaatt cccttatcca ggc 23
 39 <210> SEQ ID NO: 2
 40 <211> LENGTH: 33
 41 <212> TYPE: DNA
 42 <213> ORGANISM: Artificial Sequence
 44 <220> FEATURE:
 45 <221> NAME/KEY: primer_bind
 46 <223> OTHER INFORMATION: primer useful to clone human growth hormone cDNA
 48 <400> SEQUENCE: 2
 49 ggaaagctta gaagccacag gatccctcca cag 33
 52 <210> SEQ ID NO: 3
 53 <211> LENGTH: 16
 54 <212> TYPE: DNA
 55 <213> ORGANISM: Artificial Sequence
 57 <220> FEATURE:
 58 <221> NAME/KEY: misc_structure
 59 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
 60 with non-cohesive ends.
 62 <400> SEQUENCE: 3
 63 gataaaagatt cccaac 16
 66 <210> SEQ ID NO: 4
 67 <211> LENGTH: 17
 68 <212> TYPE: DNA
 69 <213> ORGANISM: Artificial Sequence
 71 <220> FEATURE:

PS
#2.

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72 <221> NAME/KEY: misc_structure
73 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
74 with non-cohesive ends.
76 <400> SEQUENCE: 4
77 aattgttggg aatcttt 17
80 <210> SEQ ID NO: 5
81 <211> LENGTH: 17
82 <212> TYPE: DNA
83 <213> ORGANISM: Artificial Sequence
85 <220> FEATURE:
86 <221> NAME/KEY: misc_structure
87 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
88 with non-cohesive ends.
90 <400> SEQUENCE: 5
91 ttaggcttat tcccaac 17
94 <210> SEQ ID NO: 6
95 <211> LENGTH: 18
96 <212> TYPE: DNA
97 <213> ORGANISM: Artificial Sequence
99 <220> FEATURE:
100 <221> NAME/KEY: misc_structure
101 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
102 with non-cohesive ends.
104 <400> SEQUENCE: 6
105 aattgttggg aataagcc 18
108 <210> SEQ ID NO: 7
109 <211> LENGTH: 24
110 <212> TYPE: PRT
111 <213> ORGANISM: Artificial Sequence
113 <220> FEATURE:
114 <221> NAME/KEY: SITE
115 <222> LOCATION: 1)..(19)
116 <223> OTHER INFORMATION: invertase leader sequence
118 <220> FEATURE:
119 <221> NAME/KEY: SITE
120 <222> LOCATION: 20)..(24)
121 <223> OTHER INFORMATION: first 5 amino acids of mature human serum albumin
123 <400> SEQUENCE: 7
124 Met Leu Leu Gln Ala Phe Leu Phe Leu Leu Ala Gly Phe Ala Ala Lys
125 1 5 10 15
127 Ile Ser Ala Asp Ala His Lys Ser
128 20
131 <210> SEQ ID NO: 8
132 <211> LENGTH: 21
133 <212> TYPE: DNA
134 <213> ORGANISM: Artificial Sequence
136 <220> FEATURE:
137 <221> NAME/KEY: misc_structure
138 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA

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139 fragments with non-cohesive ends.
 141 <400> SEQUENCE: 8
 142 gagatgcaca cctgagttag 21
 145 <210> SEQ ID NO: 9
 146 <211> LENGTH: 27
 147 <212> TYPE: DNA
 148 <213> ORGANISM: Artificial Sequence
 150 <220> FEATURE:
 151 <221> NAME/KEY: misc_structure
 152 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
 153 fragments with non-cohesive ends.
 155 <400> SEQUENCE: 9 27
 156 gatcctgtgg cttcgatgca cacaaga
 159 <210> SEQ ID NO: 10
 160 <211> LENGTH: 24
 161 <212> TYPE: DNA
 162 <213> ORGANISM: Artificial Sequence
 164 <220> FEATURE:
 165 <221> NAME/KEY: misc_structure
 166 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
 167 fragments with non-cohesive ends.
 169 <400> SEQUENCE: 10 24
 170 ctcttgtgtg catcgaagcc acag
 173 <210> SEQ ID NO: 11
 174 <211> LENGTH: 30
 175 <212> TYPE: DNA
 176 <213> ORGANISM: Artificial Sequence
 178 <220> FEATURE:
 179 <221> NAME/KEY: misc_structure
 180 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
 181 fragments with non-cohesive ends.
 183 <400> SEQUENCE: 11
 184 tgtggaaagag cctcagaatt tattcccaac 30
 187 <210> SEQ ID NO: 12
 188 <211> LENGTH: 31
 189 <212> TYPE: DNA
 190 <213> ORGANISM: Artificial Sequence
 192 <220> FEATURE:
 193 <221> NAME/KEY: misc_structure
 194 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
 195 fragments with non-cohesive ends.
 197 <400> SEQUENCE: 12
 198 aattgttggg aataaattct gaggctcttc c 31
 201 <210> SEQ ID NO: 13
 202 <211> LENGTH: 47
 203 <212> TYPE: DNA
 204 <213> ORGANISM: Artificial Sequence
 206 <220> FEATURE:
 207 <221> NAME/KEY: misc_structure

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208 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
 209 fragments with non-cohesive ends.

211 <400> SEQUENCE: 13

212 ttaggcttag gtggcggtgg atccggcggt ggtggatctt tcccaac 47

215 <210> SEQ ID NO: 14

216 <211> LENGTH: 48

217 <212> TYPE: DNA

218 <213> ORGANISM: Artificial Sequence

220 <220> FEATURE:

221 <221> NAME/KEY: misc_structure

222 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
 223 fragments with non-cohesive ends.

225 <400> SEQUENCE: 14

226 aattgttggg aaagatccac caccgcggta tccaccgccta cctaaggcc 48

229 <210> SEQ ID NO: 15

230 <211> LENGTH: 62

231 <212> TYPE: DNA

232 <213> ORGANISM: Artificial Sequence

234 <220> FEATURE:

235 <221> NAME/KEY: misc_structure

236 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
 237 fragments with non-cohesive ends.

239 <400> SEQUENCE: 15

240 ttaggcttag gcgggtggatctggatctg gtggcggtgg atccctccca 60
 241 ac 62

244 <210> SEQ ID NO: 16

245 <211> LENGTH: 63

246 <212> TYPE: DNA

247 <213> ORGANISM: Artificial Sequence

249 <220> FEATURE:

250 <221> NAME/KEY: misc_structure

251 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
 252 fragments with non-cohesive ends.

254 <400> SEQUENCE: 16

255 aattgttggg aaggatccac cgccaccaga tccgcgccta ccagatccac caccgcctaa 60
 256 gcc 63

259 <210> SEQ ID NO: 17

260 <211> LENGTH: 1782

261 <212> TYPE: DNA

262 <213> ORGANISM: Homo sapiens

264 <220> FEATURE:

265 <221> NAME/KEY: CDS

266 <222> LOCATION: (1)..(1755)

269 <400> SEQUENCE: 17

270 gat gca cac aag agt gag gtt gct cat cgg ttt aaa gat ttg gga gaa 48
 271 Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
 272 1 5 10 15

274 gaa aat ttc aaa gcc ttg gtg ttg att gcc ttt gct cag tat ctt cag 96
 275 Glu Asn Phe Lys Ala Leu Val Ile Ala Phe Ala Gln Tyr Leu Gln

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276	20	25	30	
278	cag tgt cca ttt gaa gat cat gta aaa tta gtg aat gaa gta act gaa			144
279	Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu			
280	35	40	45	
282	ttt gca aaa aca tgt gtt gct gat gag tca gct gaa aat tgt gac aaa			192
283	Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys			
284	50	55	60	
286	tca ctt cat acc ctt ttt gga gac aaa tta tgc aca gtt gca act ctt			240
287	Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu			
288	65	70	75	80
290	cgt gaa acc tat ggt gaa atg gct gac tgc tgt gca aaa caa gaa cct			288
291	Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro			
292	85	90	95	
294	gag aga aat gaa tgc ttc ttg caa cac aaa gat gac aac cca aac ctc			336
295	Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu			
296	100	105	110	
298	ccc cga ttg gtg aga cca gag gtt gat gtg atg tgc act gct ttt cat			384
299	Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His			
300	115	120	125	
302	gac aat gaa gag aca ttt ttg aaa aaa tac tta tat gaa att gcc aga			432
303	Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg			
304	130	135	140	
306	aga cat cct tac ttt tat gcc ccg gaa ctc ctt ttc ttt gct aaa agg			480
307	Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg			
308	145	150	155	160
310	tat aaa gct gct ttt aca gaa tgt tgc caa gct gct gat aaa gct gcc			528
311	Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala			
312	165	170	175	
314	tgc ctg ttg cca aag ctc gat gaa ctt cgg gat gaa ggg aag gct tcg			576
315	Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser			
316	180	185	190	
318	tct gcc aaa cag aga ctc aaa tgt gcc agt ctc caa aaa ttt gga gaa			624
319	Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu			
320	195	200	205	
322	aga gct ttc aaa gca tgg gca gtg gct cgc ctg agc cag aga ttt ccc			672
323	Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro			
324	210	215	220	
326	aaa gct gag ttt gca gaa gtt tcc aag tta gtg aca gat ctt acc aaa			720
327	Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys			
328	225	230	235	240
330	gtc cac acg gaa tgc tgc cat gga gat ctg ctt gaa tgt gct gat gac			768
331	Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp			
332	245	250	255	
334	agg gcg gac ctt gcc aag tat atc tgt gaa aat cag gat tcg atc tcc			816
335	Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser			
336	260	265	270	
338	agt aaa ctg aag gaa tgc tgt gaa aaa cct ctg ttg gaa aaa tcc cac			864
339	Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His			
340	275	280	285	

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
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Input Set : A:\PF548SL.txt
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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:634 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:639 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:644 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:649 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:654 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:659 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:664 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:669 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:674 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:679 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:684 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:689 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:694 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:699 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:704 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:709 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:723 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:728 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:733 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:738 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:743 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:748 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:753 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:758 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:763 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:768 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:773 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:778 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:783 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:788 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:793 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:798 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:812 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:817 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:822 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:827 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:832 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:837 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:842 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:847 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:852 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:857 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:862 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:867 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:872 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:877 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:882 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27

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L:887 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:902 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28
L:907 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28
L:912 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28
L:917 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28
L:922 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28
L:977 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1181 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:1284 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33